

FIG. 4

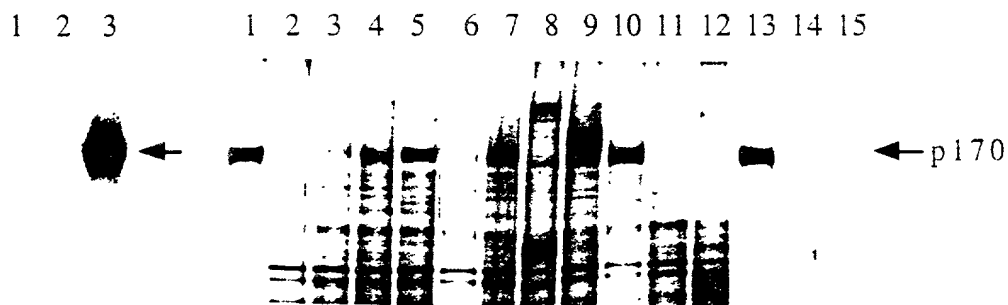


FIG. 5A

FIG. 5B

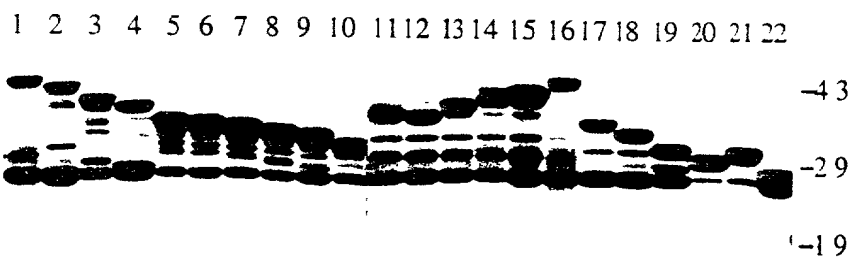


FIG. 7A

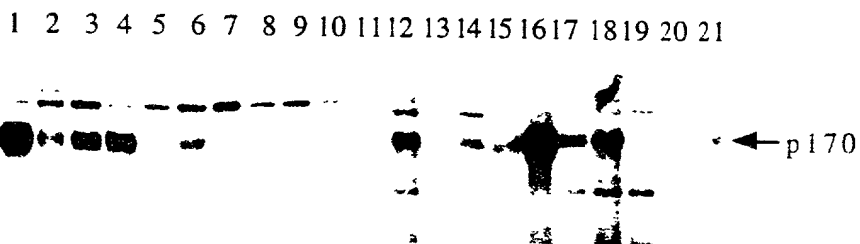


FIG. 7B

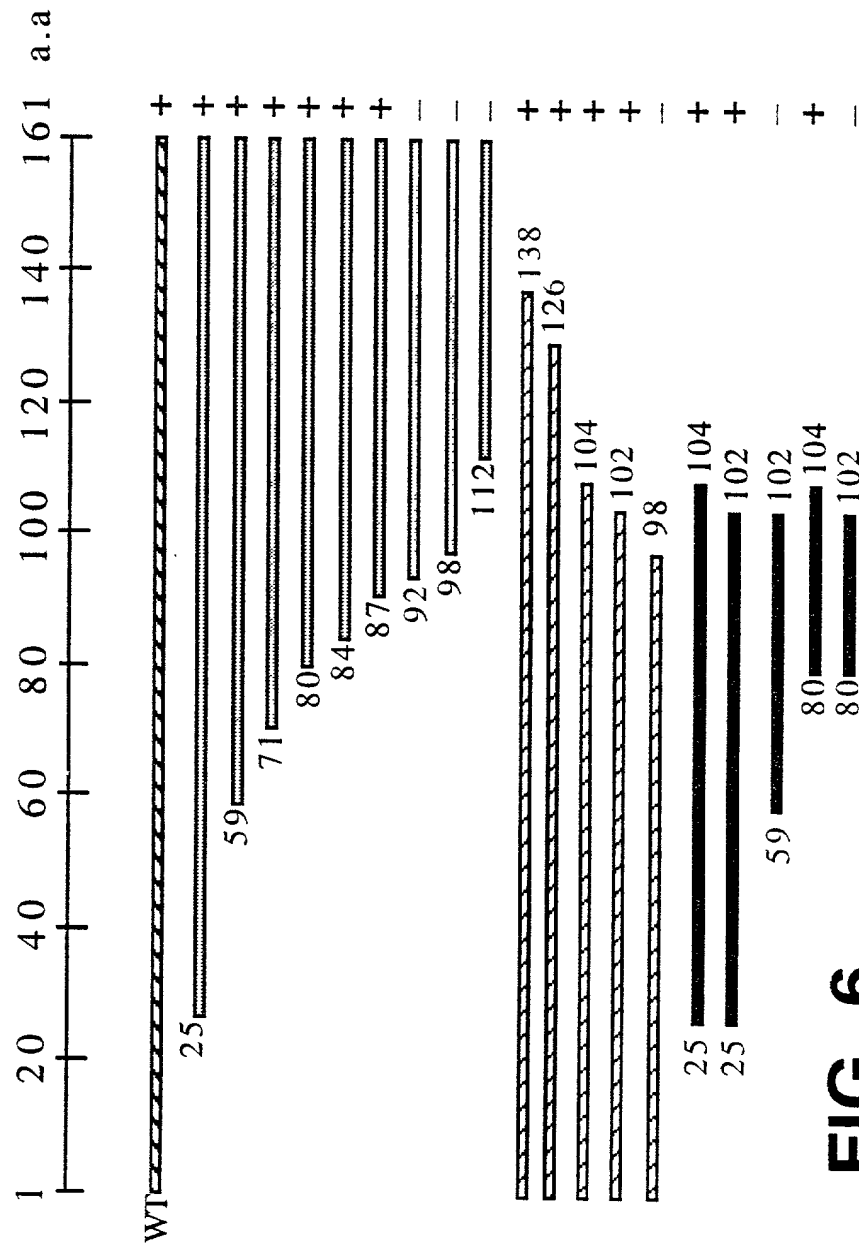


FIG. 6

DHBV pre-S region

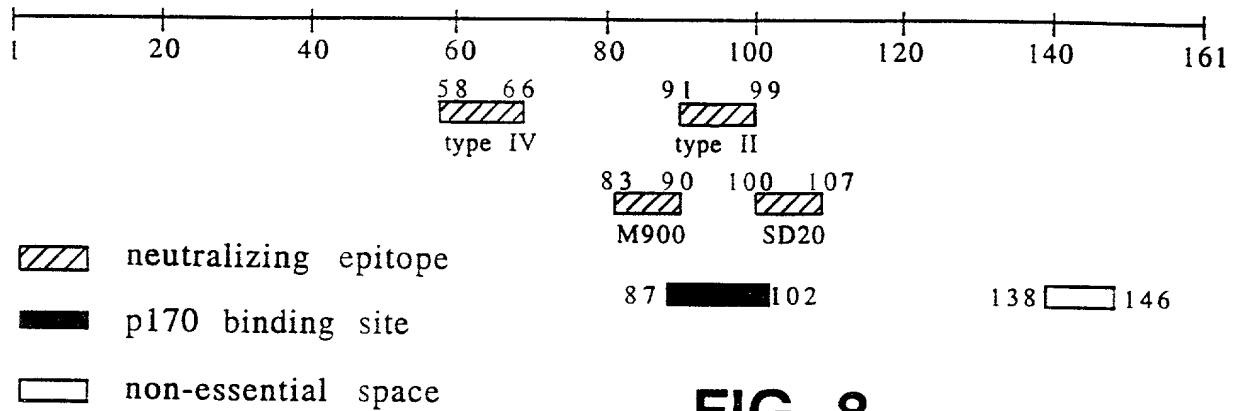


FIG. 8

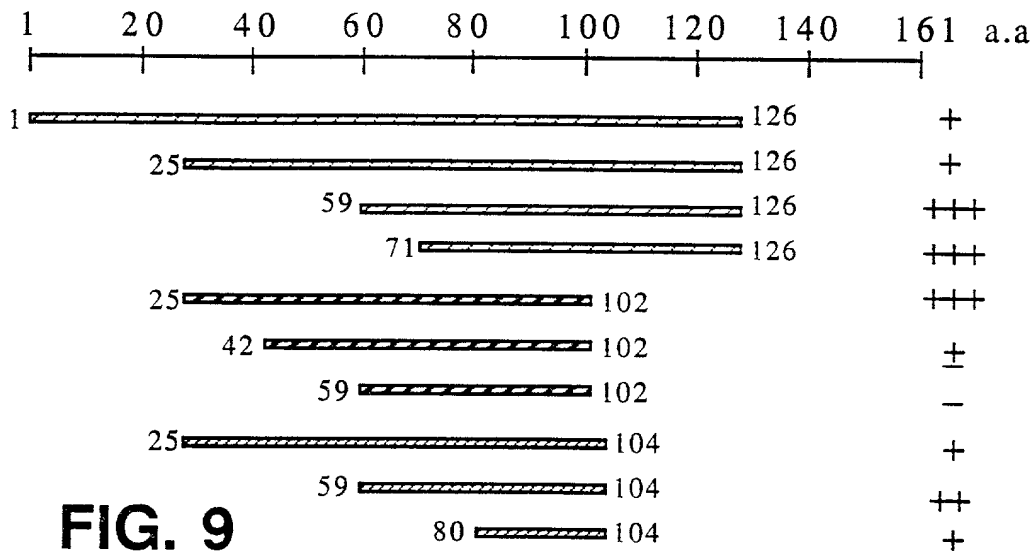


FIG. 9

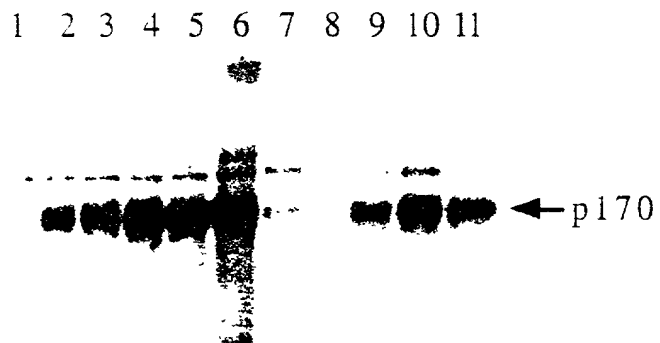


FIG. 10

A pre-S polypeptide containing p170 binding site blocks DHBV infectivity

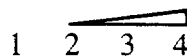


FIG. 11

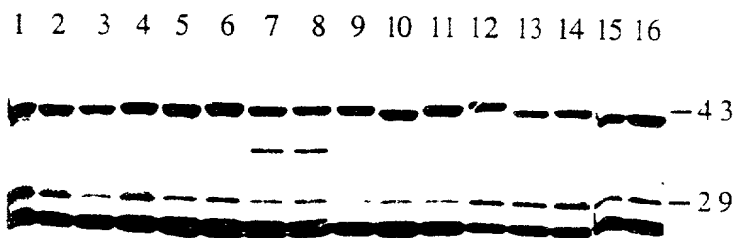


FIG. 13A

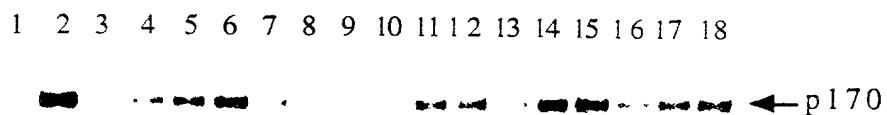


FIG. 13B

	87	90	93	96	99	102										
wild-type	Q	W	T	P	E	E	D	Q	K	A	R	E	<u>A</u>	F	R	R
W88S		S														
P90L			L													
E91G				G												
E92V					V											
D93F						F										
K95S								S								
R97L										L						
R97C										C						
E98A											A					
E98V											V					
R102G															G	
E91G/K95S				G				S								
E91G/R97C				G						C						
K95S/A96T								S	T							
K95S/R97C								S		C						
K95S/R97L/E98A								S		L	A					

FIG. 12

peptide 1	SVELRELYVMEISDNPGVHEAGEPEFK (SEQ ID NO:19)
peptide 2	LIDRTRIVIVPSLNPDGR-IA (SEQ ID NO:20)
peptide 3	SLLSHEFQDETDTTEEETLYSAK (SEQ ID NO:21)
peptide 4	VEEGKVPVLNTPD (SEQ ID NO:22)

FIG. 14A

peptide 1	SVELRELYVMEISDNPGVHEAGEPEFK (SEQ ID NO:19)
bovine CPH	.F.G...L.L.L.....P.....
human CPH	.F.G...L.I.L.....P.....
AEBP1 gene	KI.A.....D..L.....R
human CPN	...G.H...L.F..H..I..PL...V.
human CPM	..KG.N.W.LVVGRF.KE.RI.I....

peptide 2	LIDRTRIVIVPSLNPDGR-IA (SEQ ID NO:20)
AEBP1 gene	.VQD...HL.....YEV.
bovine CPH	..HN...H.M.....
human CPN	..QD...H.L..M....YEV.
human CPM	..NS...H.M..M....
human CPH	..HS...H.M.....

FIG. 14B

1/1	ATG GGG CAA CAT CCA GCA AAA TCA ATG GAC GTC AGA CGG ATA GAA GGA GGA GAA ATA CTG	(SEQ ID NO:33)
M G	Q Q H P A K S M D V R R I E G G E I L	(SEQ ID NO:34)
61/21	TTA AAC CAA CTT GCC GGA AGG ATG ATC CCA AAA GGG ACT TTG ACA TGG TCA GGC AAG TTT	
L N	Q Q L A G R M I P K G T L T W S G K F	
121/41	CCA ACA CTA GAT CAC GTG TTA GAC CAT GTG CAA ACA ATG GAG GAG ATA AAC ACC CTC CAG	
P T	L D H V L D H V Q T M E I N T L Q	
181/61	AAT CAG GGA GCT TGG CCT GCT GGG GCG GGA AGG AGA GTA GGA TTA TCA AAT CCG ACT CCT	
N Q	G A W P A G A G R R V G L S N P T P	
241/81	CAA GAG ATT CCT CAG CCC CAG TGG ACT CCC GAG GAA GAC CAA AAA GCA CGC GAA GCT TTT	
Q E	I P Q P Q W T P E E D Q K A R E A F	
301/101	CGC CGT TAT CAA GAA GAA AGA CCA CCG GAA ACC ACC ACC ATT CCT CCG TCT TCC CCT CCT	
R R	Y Q E E R P P E T T I P P S S P P	
361/121	CAG TGG AAG CTA CAA CCC GGG GAC GAT CCA CTC CTG GGA AAT CAG TCT CTC CTC GAG ACT	
Q W	K L Q P G D D P L L G N Q S L L E T	
421/141	CAT CCG CTA TAC CAG TCA GAA CCA CCG GTG CCA GTG ATA AAA ACT CCC CCC TTG AAG AAG	
H P	L Y Q S E P A V I K T P P L K K	
481/161	AAA	
	K	

FIG. 16

FIG. 17A

FIG. 17B

FIG. 17C

FIG. 17D

FIG. 17E

FIG. 17

[illegible]

FIG. 17A

[illegible]

Pres2	120	174
PHBV3200	USA	adw2
PHBV933	USA	adw2
PRDW294	the Philippines	adw2
PMWD122	Indonesia	adw2
PRTB299	Indonesia	adw2
POOW282	Japan	adw2
PJDW233	Japan	adw2
PAK66	Japan	adw
-K619	Japan	adw
BV1-1	Japan	adr
PRRH8adr4	Japan	adr
PHBr330	Japan	adr
PADRRho	Korea	adr
ADRRen	China	adr
PRB259	Japan	ayr
HMA	New Caledonia	adrq-
Cha	Polynesia	adrq-
PHBV320	Latvia	ayw2
aywmut	Italy	ayw2
HBValpha1	Turkey	ayw2
PPYW310	Papua	ayw2
EcoHBVDNA	France	ayw3
PRWB796	Japan	ayw3
Bas	West Africa	ayw4
Kou	Senegal	ayw4
Fou	France	adw4
9203/85	Colombia	adw4
adw/LSH	chimpanzee	

FIG. 17C

[illegible]

FIG. 17D

[illegible]

FIG. 17E

1/1
 ATG GAG ATC TCG GAC AAC CCC GGT GTT CAT GAA GCA GGT GAG CCA GAG TTC AAG TAT ATT
 M E I S D N P G V H E A G E P E F K Y I

61/21
 GGT AAC ATG CAT GGG AAT GAA GTT GTG GGG CGA GAG CTG CTC CTG AAC CTC ATC GAG TAC
 G N M H G N E V V G R E L L L N L I E Y

121/41
 CTC TGC AAG AAC TTC GGC ACA GAT CCC GAA GTG ACT GAC TTG GTC CAG AGC ACG CGG ATC
 L C K N F G T D P E V T D L V Q S T R I

181/61
 CAC ATC ATG CCG TCC ATG AAC CCA GAT GGC TAC GAG AAG TCC CAG GAA GGA GAC AGA GGA
 H I M P S M N P D G Y E K S Q E G D R G

241/81
 GGC ACC GTT GGC AGA AAT AAC AGC AAC AAC TAC GAC CTG AAC CGG AAC TTC CCA GAT CAG
 G T V G R N N S N N Y D L N R N F P D Q

301/101
 TTC TTC CAG GTG ACA GAC CCT CCG CAG CCA GAA ACT CTT GCT GTC ATG AGC TGG TTG AAA
 F F Q V T D P P Q P E T L A V M S W L K

361/121
 ACT TAC CCG TTC GTG CTT TCA GCA AAC CTG CAT GGA GGT TCT CTG GTG GTT AAT TAC CCT
 T Y P F V L S A N L H G G S L V V N Y P

421/141
 TTT GAT GAC GAT GAA CAA GGA ATA GCC ATA TAC AGT AAA TCC CCA GAC GAT GCT GTG TTT
 F D D D E Q G I A I Y S K S P D D A V F

481/161
 CAG CAG CTG GCA CTT TCC TAC TCC AAG GAA AAC AAA AAG ATG TAT CAG GGA AGC CCT TGT
 Q Q L A L S Y S K E N K K M Y Q G S P C

541/181
 AAG GAT TTG TAC CCC ACA GAG TAC TTT CCA CAT GGC ATC ACG AAC GGG GCC CAG TGG TAC
 K D L Y P T E Y F P H G I T N G A Q W Y

601/201
 AAC GTT CCA GGT GGG ATG CAG GAC TGG AAT TAC TTA AAT ACC AAC CTG TTT GAA GTG ACC
 N V P G G M Q D W N Y L N T N L F E V T

661/221
 ATT GAG CTG GGC TGT GTG AAA TAC CCA AAA GCA GAG GAG CTG CCG AAG TAC TGG GAG CAG
 I E L G C V K Y P K A E E L P K Y W E Q

721/241
 AAC CGT AGA TCT CTC CTC CAG TTC ATT AAA CAG GTT CAC CGC GGC ATC TGG GGA TTT GTG
 N R R S L L Q F I K Q V H R G I W G F V

781/261
 CTG GAT GCC ACG GAC GGA AGG GGC ATT CTC AAC GCC ACC ATC AGC GTC GCC GAC ATC AAC
 L D A T D G R G I L N A T I S V A D I N

841/281
 CAC CCC GTG ACC ACC TAC AAA GAT GGG GAC TAC TGG CGC CTC TTG GTC CAG GGG ACG TAC
 H P V T T Y K D G D Y W R L L V Q G T Y

901/301
 AAA GTC ACA GCA TCT GCC CGA GGG TAT GAT CCA GTC ACT AAA ACG GTG GAA GTC GAC AGC
 K V T A S A R G Y D P V T K T V E V D S

961/321
 AAA GGT GGG GTG CAG GTC AAC TTC ACT CTT TCA CGG ACA GAC GCC AAA GTG GAG GAG GGG
 K G G V Q V N F T L S R T D A K V E E G

1021/341
 AAG GTG CCA GTC CTG AAC ACC CCA GAC ACC AGC GAC CCC AAC GAG AAG GAG TTT GAG ACT
 K V P V L N T P D T S D P N E K E F E T

1081/361
 CTG ATC AAA GAT CTA TCT GCT GAA AAC GGC CTG GAG (SEQ ID NO:63)
 L I K D L S A E N G L E (SEQ ID NO:64)

FIG. 18

1/1
 TTT GTC CAG GAC AAG AGT GGC AAG GCA ATT TCT AAA GCT ACC ATT GTC CTT AAT GAA GGC
 F V Q D K S G K A I S K A T I V L N E G
 61/21
 TTG AGG GTC TAC ACT AAA GAA GGT GGC TAT TTC CAT GTG CTG TTG GCT CCT GGT TTG CAT
 L R V Y T K E G G Y F H V L A P G L H
 121/41
 AAC ATC AAT GCG ATA GCG GAT GGG TAC CAA CAA AAG CAT ATG AAG GTC TTG GTA CGC CAC
 N I N A I A D G Y Q Q K H M K V L V R H
 181/61
 GAT GCA CCC AGC TCT GTG TTC ATG GTA TTT GAC ATG GAA AAC AGG ATA TTT GGT CTG CCT
 D A P S S V F M V F D M E N R I F G L P
 241/81
 CGA GAG CTG GTT GTA ACT GTT GCA GGT GCA ATT ATG TCT GCT TTG GTC CTC ACT GCC TGT
 R E L V V T V A G A I M S A L V L T A C
 301/101
 ATC ATC TGG TGT GTC TGC TCA ATC AAG GCC AAC AGA CAC AAA GAT GGC TTC CAC TGC CGG
 I I W C V C S I K A N R H K D G F H C R
 361/121
 CAG CAC CAC GAC GAT TAC GAG GAC GAA ATC CGC ATG ATG TCC ACT GGC TCA AAG AAA TCC
 Q H H D D Y E D E I R M M S T G S K K S
 421/141
 CTT TTG AGC CAC GAA TTC CAG GAT GAA ACA GAC ACT GAA GAA (SEQ ID NO:65)
 L L S H E F Q D E T D T E E (SEQ ID NO:66)

FIG. 19

HBV (SEQ ID NO:67)
DHBV (SEQ ID NO:68)

71	HBV	H	G	G	I	L	G	W	S	P	Q	A	Q	G	I	L	T	T	V	S	T	I	P	P	P	A	S	T	N	R	Q	S	G	R	Q	P	T	P	I	S	P	P	L	R	D	S	H	P	Q	118
69	DHBV	A	G	R	R	V	G	L	S	N	P	T	P	Q	E	I	P	Q	P	Q	W	T	P	E	E	D	Q	K	A	R	E	A	F	R	R	Y	Q	E	E	R	P	P	E	T	T	I	P	P	116	
		*		*		*		*		*		*		*		*		*		*		*		*		*		*		*		*		*		*		*		*		*		*		*				

HBV (SEQ ID NO:67)
DHBV (SEQ ID NO:68)

p170 binding site

FIG. 20

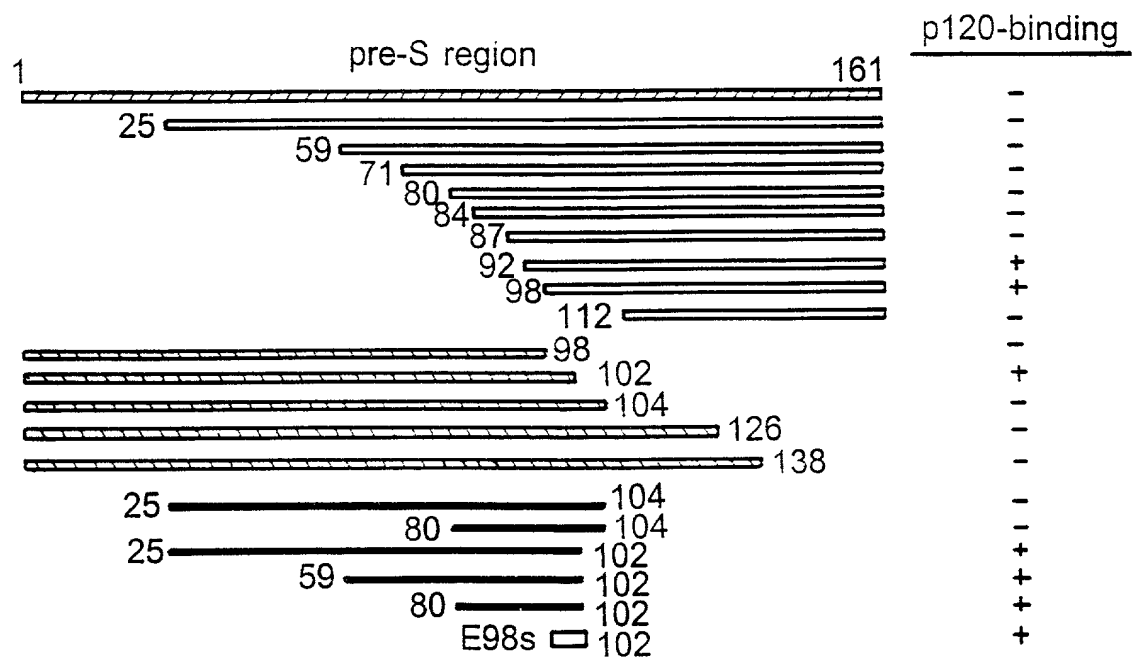


FIG. 21A

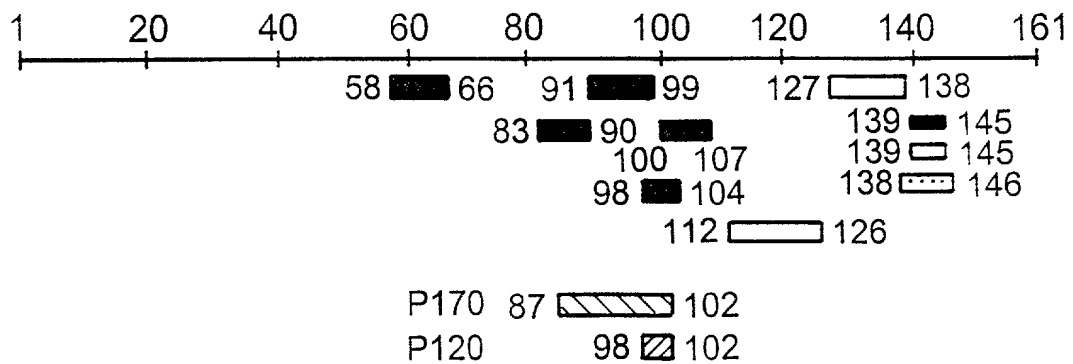


FIG. 22

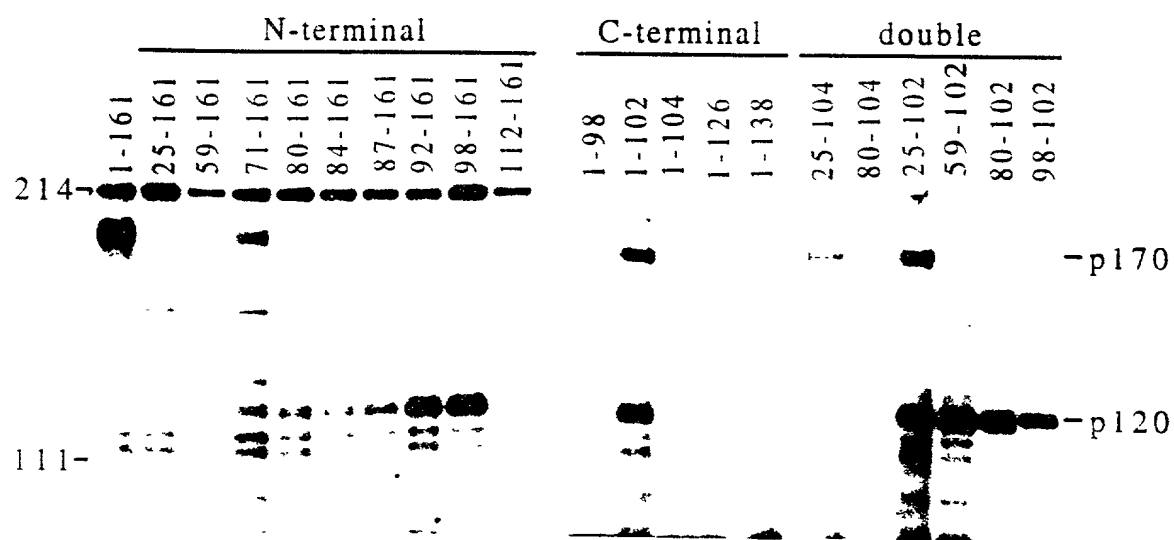


FIG. 21B

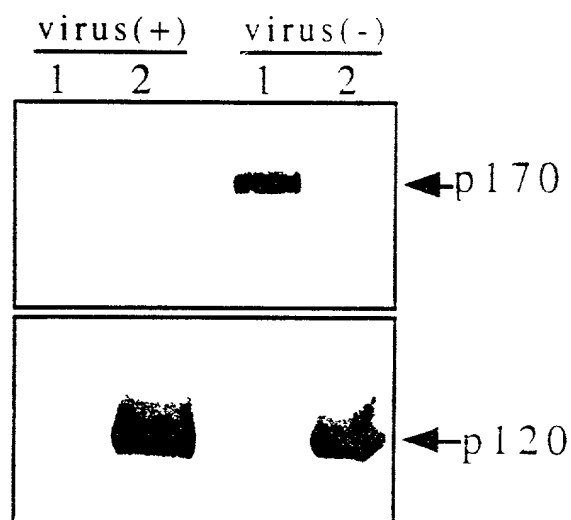


FIG. 23

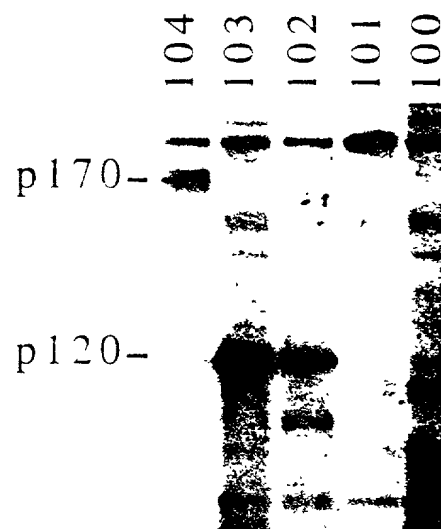


FIG. 24

			97	98	99	100	101	102	<u>p120-binding</u>
WT	Lys	Ala	Arg	Glu	Ala (Tyr)	Phe	Arg	Arg	+
R97C			Cys						+
E98V				Val					+
E98A				Ala					+
A99D					Asp				+
F100V						Val			-
F100L						Leu			-
F100W						Trp			+
R101L							Leu		-
R101H							His		-
R101K							Lys		+ weak
R102G								Gly	-
R102H								His	-
R102K								Lys	-

FIG. 25A

peptide 1: DVSGVLFQYPDTEGK (SEQ ID NO:70)

peptide 2: EVYRLALQTREQHIRRD (SEQ ID NO:71)

peptide 3: SGAQGEYAGLAAIK (SEQ ID NO:72)

peptide 4: IQPIEVDK (SEQ ID NO:73)

Peptide sequences of p120.

FIG. 30

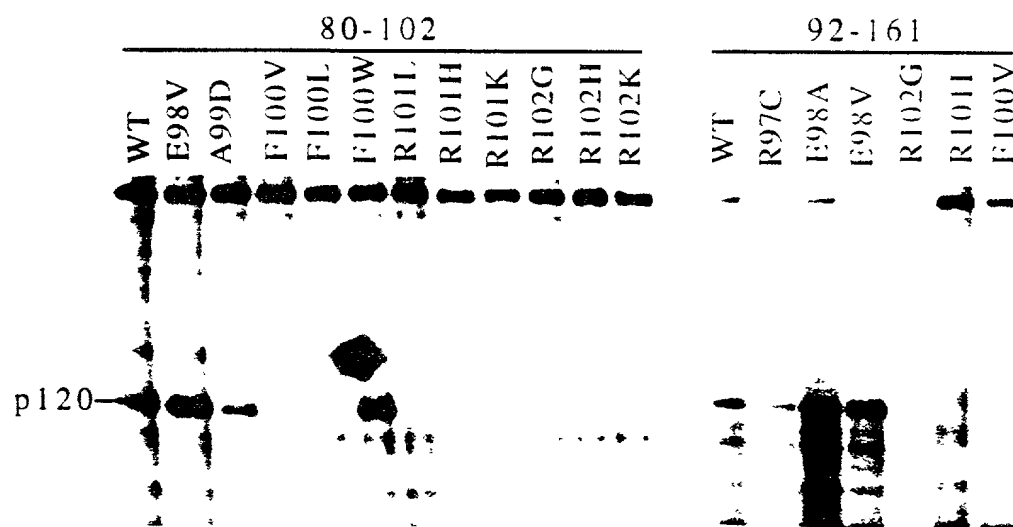


FIG. 25B

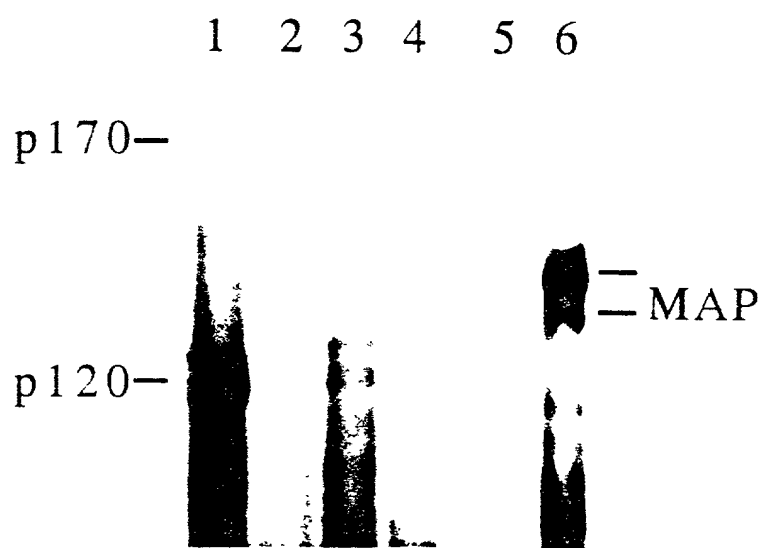


FIG. 26

1 2 3 4 5 6

FIG. 27A



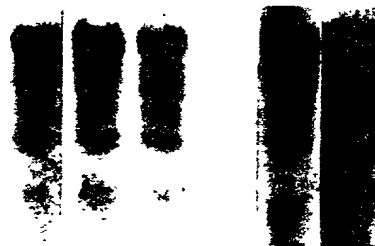
FIG. 27B



FIG. 27C



FIG. 27D



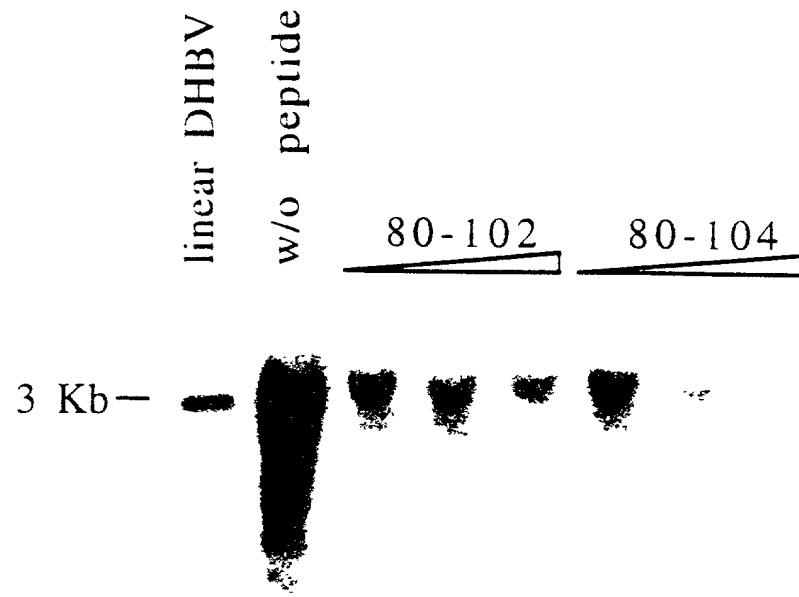


FIG. 28

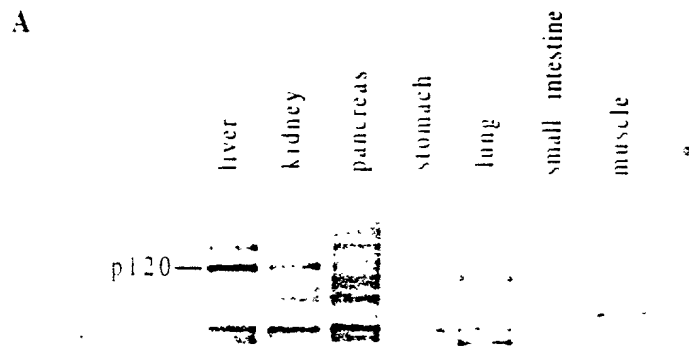


FIG. 29A

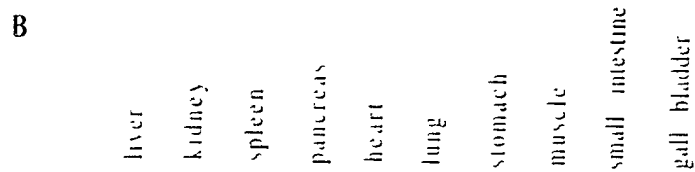


FIG. 29B

1/1
 31/11
 GAG GCG GCG CGG TGC ATC GAG CAG CTG CTG CCG CGG CAC GAT GAC TTC TCC CGG CGG CAC
 E A A R C I E Q L L P R H D D F S R R H
 61/21
 91/31
 ATC GGC CCC CGG GAG GGG GAG AAG AGG GAG ATG CTG CGA GCC CTC GGG GTG CAG AGC GTC
 I G P R E G E K R E M L R A L G V Q S V
 121/41
 151/51
 GAG GAG CTG ATG GAT AAA GCC ATC CCG GGC AGC ATC CGG CTG CGC AGG CGG CTG AGG ATG
 E E L M D K A I P G S I R L R R P L R M
 181/61
 211/71
 GAG GAC CCC GTG GGT GAA AAT GAA ATC CTT GAA ACT TTA TAC AAT AAT GCA AGC AAG AAC
 E D P V G E N E I L E T L Y N I A S K N
 241/81
 271/91
 AAG ATA TGG AGG TCC TAT ATA GGC ATG GGT TAT TAC AAC TGC TCA GTG CCT CAA CCC ATT
 K I W R S Y I G M G Y Y N C S V P Q I
 301/101
 331/111
 GCA CGG AAT TTG TTG GAG AAT GCA GGA TGG GTT ACC CAG TAT ACT CCC TAC CAA CCT GAG
 A R N L L E N A G W V T Q Y T P Y Q P E
 361/121
 391/131
 GTC TCA CAG GGC AGG CTG GAG AGC CTG CTA AAT TAC CAG ACT ATG GTG TGT GAT ATC ACA
 V S Q G R L E S L L N Y Q T M V C D I T
 421/141
 451/151
 GGA ATG GAT GTG GCT AAT GCA TCA TTG CTG GAT GAG GGG ACA GCT GCT GCA GAA GCT ATG
 G M D V A N A S L L D E G T A A A E A M
 481/161
 511/171
 CAA TTA TGT CAC AGG CAC AAC AAA AGG AGG AAG TTT TAT GTA GAT TCC CGA TGC CAC CCT
 Q L C H R H N K R R K F Y V D S R C H P

FIG. 31A

541/181
 CAG ACT ATA GCA GTG GTC CAA ACT AGA GCC AAT TAT ACA GGT GTT ATT ACT GAG CTC AAA
 Q T I A V V Q T R A N Y T G V I T E L K
 601/201
 TTA CCC CAT GAG ATG GAT TTC AGT GGA AAG GAT GTC AGT GGA GTA TTA TTT CAG TAT CCA
 L P H E M D F S G K D V S G V L F Q Y P
 661/221
 GAC ACT GAG GGG AAG GTG GAA GAC TTC TCT GAA CTT GTT GAA AGA GCT CAT CAG AAC GGG
 D T E G K V E D F S E L V E R A H Q N G
 721/241
 ACT CTT GCC TGC TGT GCT ACT GAT CTT CTG GCT CTC TGT ATT CTG AAG CCT CCT GGA GAG
 T L A C C A T D L L A L C I L K P P G E
 781/261
 TTT GGG GTA GAT GTT GTC CTG GGT AGC TCC CAG AGA TTT GGT GTG CCA CTC TGC TAT GGG
 F G V D V V L G S S Q R F G V P L C Y G
 841/281
 GGA CCC CAC GCA GCA TTC TTT GCT GTC AAG GAA AAC CTA GTG AGA ATG ATG CCA GGC AGG
 G P H A A F F A V K E N L V R M M P G R
 901/301
 ATG GTG GGT GTC ACA AGA GAT GCA AAT GGA AAA GAA GTT TAC CGA CTG GCT TTA CAA ACA
 M V G V T R D A N G K E V Y R L A L Q T

FIG. 31B

961/321 CGA GAG CAG CAT ATC AGG AGG GAC AAA GCT ACA AGC AAC ATC TGC ACA GCA CAG GCT CTT
 R E Q H I R R D K A T S N I C T A Q A L
 1021/341 1051/351
 CTG GCT AAT ATG GCA GCC ATG TTT GGT GTC TAC CAT GGG TCT GAT GGA TTA AGG GAT ATT
 L A N M A A M F G V Y H G S D G L R D I
 1081/361 1111/371
 GCA AGA CGG GTA CAC AAT GCT ACT TTA ATC CTG GCT GAA GGT CTC AGG AGA GCT GGT CAT
 A R R V H N A T L I L A E G L R R A G H
 1141/381 1171/391
 AAA CTG CAC CAT GAT CTG TTC TTT GAT ACC TTG ACA GTC ACG TGT GGA TGC TCA GTC AAA
 K L H H D L F F D T L T V T C G C S V K
 1201/401 1231/411
 GAA GTT TTG GAC AGG GCA GCT CTT AGA AAG ATA AAT TTT CGC ATT TAT AGT GAT GCC AGA
 E V L D R A A L R K I N F R I Y S D G R
 1261/421 1291/431
 CTT CGA GTA TCA CTT GAT GAA ACT GTA AGT GAG AAA GAC CTA GAT GAC ATA TTA TGG ATT
 L G V S L D E T V S E K D L D D I L W I
 1321/441 1351/451
 TTT GGT TGC GAG TCT TCA GCT GAA CTA ATT GCT GAA GGT ATG GGC GAG GAA ACC AAA GGT
 F G C E S S A E L I A E G M G E E T K G
 1381/461 1411/471
 ATC CTT AGC ACC CCA TTT AAG AGA ACT TCC AAA TTC TTG ACC CAT CAG GTT TTC AAC AGC
 I L S T P F K R T S K F L T H Q V F N S

FIG. 31C

1441/481
TAT CAC TCC GAA ACA AAT ATC GTA CGG TAC ATG AAG AGA TTA GAA AAC AAA GAT ATT TCC
Y H S E T N I V R Y M K R L E N K D I S
1501/501
CTT GTT CAC AGC ATG ATT CCT TTG GGG TCC TGT ACA ATG AAG CTC AAT AGT TCA GCT GAA
L V H S M I P L G S C T M K L N S S A E
1561/521
CTT GCA CCT ATT TCA TGG AAG GAA TTT GCC AAC ATC CAC CCC TTT GTG CCC TTG GAT CAA
L A P I S W K E F A N I H P F V P L D Q
1621/541
GCT CAA GGG TAT CAG CAG CTT TTC AAG GAC TTA GAG AAG GAC CTG TGT GAG ATT ACT GGT
A Q G Y Q Q L F K D L E K D L C E I T G
1681/561
TAC GAC AAA ATC TCC TTC CAA CCA AAC AGT GGA GCC CAA GGA GAG TAC GCA GGC TTG GCC
Y D K I S F Q P N S G A Q G E Y A G L A
1741/581
GCA ATC AAA GCT TAT TTA AAT GCA AAA GGA GAA CGT CAT CGA AGT GTT TGC CTT ATT CCT
A I K A Y L N A K G E R H R S V C L I P
1801/601
AGA TCT GCT CAT GGT ACA AAT CCA GCA AGT GCA CAG ATG GCA GGG ATG AAG ATT CAA CCA
R S A H G T N P A S A Q M A G M K I Q P

1471/491
1531/511
1591/531
1651/551
1711/571
1771/591
1831/611

FIG. 31D

1861/621
GTT GAA GTA GAT AAA AAT GGG AGC ATT GAT ATC TCC CAT TTA AAA GCA ATG GTG GAC AAA
V E V D K N G S I D I S H L K A M V D K

1921/641
CAC AAG GAG AAC CTG GCA GCC ATC ATG ATC ACA TAC CCT TCC ACC AAT GGT GTG TTT GAG
H K E N L A A I M I T Y P S T N G V F E

1891/631
1951/651
2011/671
GAG GAG ATT GGG GAT GTG TGT GAG CTG ATT CAC AAA AAC GGA GGC CAG GTT TAC CTG GAT
E E I G D V C E L I H K N G G Q V Y L D

2041/681
GGA GCA AAC ATG AAC GCC CAA GTG GGT CTG TGT CGT CCT GGA GAT TAT GGC TCT GAT GTC
G A N M N A Q V G L C R P G D Y G S D V

2101/701
TCT CAC TTA AAC CTT CAC AAA ACC TTT TGC ATT CCC CAT GGA GGA GGA CCT GGA ATG
S H L N L H K T F C I P H G G G G P G M

2161/721
GGA CCA ATT GGA GTG AAG AAA CAT CTG GCT CCC TAC TTG CCT ACC CAT CCT GTC ATC AAG
G P I G V K K H L A P Y L P T H P V I K

FIG. 31E

2221/741
ATT CAG ACG GAT AAG GAT GCA TGT CCT TTG GGT ACT GTC AGT GCT GCA CCT TGG GGT TCC
I Q T D K D A C P L G T V S A A P W G S

2281/761
AGT GCT ATA TTG CCT ATT TCC TGG GTG TAT ATC AAG ACA ATG GGA GCA AAG GGT CTT AAA
S A I L P I S W V Y I K T M G A K G L K

2341/781
CAC GCT TCT GAG GTT GCT ATA TTA AAT GCA AAC TAC ATG GCA AAG AGG CTG GAG AAG CAC
H A S E V A I L N A N Y M A K R L E K H

2401/801
TAC AAA ATC CTT TTC AGA GGA GTA AGA GGT TAT GTA GCC CAT GAA TTC ATT TTG GAT ACA
Y K I L F R G V R G Y V A H E F I L D T

2461/821
AGA CCT TTC AAA ACA GCA AAC ATT GAA GCT GTG GAT CTT GCT AAG CGA CTT CAG GAT
R P F K K T A N I E A V D L A K R L Q D

2521/841
TAT GGT TTT CAT GCT CCA ACC ATG TCC TGG CCA GTG GCA GGC ACA CTT ATG ATT GAA CCA
Y G F H A P T M S W P V A G T L M I E P

2581/861
ACA GAG TCT GAA GAC AAG GCA GAG CTG GAC ACG TTT TGT GAT GCA ATG ATC AGT ATT CGA
T E S E D K A E L D R F C D A M I S I R

2251/751
2311/771
2371/791
2431/811
2491/831
2551/851
2611/871

FIG. 31F

2641/881
CAG GAA ATT GCT GAA ATA GAG GAG GGC AGG ATG GAC CCT CAG ATT AAC CCA TTA AAG ATG
Q E I A E I E E G R M D P Q I N P L K M
2701/901
TCA CCA CAT ACT CTA AAC TGT GTC ACT TCT TCA AAG TGG GAT CGT CCT TAT TCC AGA GAA
S P H T L N C V T S S K W D R P Y S R E
2761/921
GTG GCA GCA TTC CCA CTG CCG TTT GTG AAA CCT GAG AGC AAG TTT TGG CCC ACA ATT GCT
V A A F P L P F V K P E S K F W P T I A
2821/941
CGC ATC GAT GAC ATA TAC GGA GAT CAA CAC CTG GTT TGT ACC TGC CCA CCG ATG GAA GCC
R I D D I Y G D Q H L V C T C P P M E A
2881/961
TAC GAA TCT CCC TTC TCT GAA CAG AAG AGA GCA TCT TCG TAA (SEQ ID NO:74)
Y E S P F S E Q K R A S S * (SEQ ID NO:75)

FIG. 31G